

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(1.1) NUMBER OF SEQUENCES: 14

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGCCCAGCTC CTGCCCCGCC GCTT

24

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGCATCAAC ACAGGCGCCT CTTC

24

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTCAAATGAG ATTGTGGGAA AATTGCT

27

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGATCATCTC TGCCTGAGTA TCTT

24

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCACCCATGG CAAATTCCAT GGCA

24

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCTAGACGOC AGGTCAGGTC CACC

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: protein

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Asp Ile Asp Pro Thr Val Leu Leu Lys Glu Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTGCGATGCT CGCCCGCGCC CTG

23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CITCTACAGT TCAOTCGAAC GTTC

24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
1      5      10      15
Thr Ala Asn Pro Cys Cys Ser His Pro Cys Glu Asn Arg Gly Val Cys
20      25      30
Met Ser Val Gly Phe Asp Glu Tyr Lys Cys Asp Cys Thr Arg Thr Gly
35      40      45
Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
50      55      60
Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
65      70      75      80
Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
85      90      95
Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
100      105      110
Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
115      120      125
Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
130      135      140
Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Glu Leu Pro Asp Ser
145      150      155      160
Asn Glu Ile Val Glu Lys Leu Leu Leu Arg Arg Lys Phe Ile Pro Asp
165      170      175
Pro Glu Gly Ser Asn Met Met Phe Ala Phe Phe Ala Glu His Phe Thr
180      185      190
His Glu Phe Phe Lys Thr Asp His Lys Arg Gly Pro Ala Phe Thr Asn
195      200      205
Gly Leu Gly His Gly Val Asp Leu Asn His Ile Tyr Gly Glu Thr Leu
210      215      220
Ala Arg Glu Arg Lys Leu Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr
225      230      235      240
Glu Ile Ile Asp Gly Glu Met Tyr Pro Pro Thr Val Lys Asp Thr Glu
245      250      255
Ala Glu Met Ile Tyr Pro Pro Glu Val Pro Glu His Leu Arg Phe Ala
260      265      270
Val Gly Glu Glu Val Phe Gly Leu Val Pro Gly Leu Met Met Tyr Ala
275      280      285
Thr Ile Trp Leu Arg Glu His Asn Arg Val Cys Asp Val Leu Lys Glu
290      295      300
Glu His Pro Glu Trp Gly Asp Glu Glu Leu Phe Glu Thr Ser Arg Leu
305      310      315      320
Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Glu
325      330      335
His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu

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| 340 | | | | | | 345 | | | | | | 350 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Phe | Asn | Lys | Gln | Phe | Gln | Tyr | Gln | Asn | Arg | Ile | Ala | Ala | Gln | Phe | Asn | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | |
| Thr | Leu | Tyr | His | Trp | His | Pro | Leu | Leu | Pro | Asp | Thr | Phe | Gln | Ile | His | | |
| | | 370 | | | | 375 | | | | | 380 | | | | | | |
| Asp | Gln | Lys | Tyr | Asn | Tyr | Gln | Gln | Phe | Ile | Tyr | Asn | Asn | Ser | Ile | Leu | | |
| | | 385 | | | 390 | | | | | 395 | | | | | 400 | | |
| Leu | Glu | His | Gly | Ile | Thr | Gln | Phe | Val | Gln | Ser | Phe | Thr | Arg | Gln | Ile | | |
| | | | | 405 | | | | | 410 | | | | | 415 | | | |
| Ala | Gly | Arg | Val | Ala | Gly | Gly | Arg | Asn | Val | Pro | Pro | Ala | Val | Gln | Lys | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |
| Val | Ser | Gln | Ala | Ser | Ile | Asp | Gln | Ser | Arg | Gln | Met | Lys | Tyr | Gln | Ser | | |
| | | 435 | | | | | 440 | | | | | 445 | | | | | |
| Phe | Asn | Gln | Tyr | Arg | Lys | Arg | Phe | Met | Leu | Lys | Pro | Tyr | Gln | Ser | Phe | | |
| | | 450 | | | | 455 | | | | | 460 | | | | | | |
| Gln | Glu | Leu | Thr | Gly | Glu | Lys | Gln | Met | Ser | Ala | Gln | Leu | Gln | Ala | Leu | | |
| | | | | | 470 | | | | | 475 | | | | | 480 | | |
| Tyr | Gly | Asp | Ile | Asp | Ala | Val | Gln | Leu | Tyr | Pro | Ala | Leu | Leu | Val | Gln | | |
| | | | | 485 | | | | | 490 | | | | | 495 | | | |
| Lys | Pro | Arg | Pro | Asp | Ala | Ile | Phe | Gly | Gln | Thr | Met | Val | Gln | Val | Gly | | |
| | | | 500 | | | | | 505 | | | | | 510 | | | | |
| Ala | Pro | Phe | Ser | Leu | Lys | Gly | Leu | Met | Gly | Asn | Val | Ile | Cys | Ser | Pro | | |
| | | 515 | | | | | 520 | | | | | 525 | | | | | |
| Ala | Tyr | Trp | Lys | Pro | Ser | Thr | Phe | Gly | Gly | Gln | Val | Gly | Phe | Gln | Ile | | |
| | | 530 | | | | 535 | | | | | 540 | | | | | | |
| Ile | Asn | Thr | Ala | Ser | Ile | Gln | Ser | Leu | Ile | Cys | Asn | Asn | Val | Lys | Gly | | |
| | | | | | 550 | | | | | 555 | | | | | 560 | | |
| Cys | Pro | Phe | Thr | Ser | Phe | Ser | Val | Pro | Asp | Pro | Gln | Leu | Ile | Lys | Thr | | |
| | | | | 565 | | | | | 570 | | | | | 575 | | | |
| Val | Thr | Ile | Asn | Ala | Ser | Ser | Ser | Arg | Ser | Gly | Leu | Asp | Asp | Ile | Asn | | |
| | | | 580 | | | | | 585 | | | | | 590 | | | | |
| Pro | Thr | Val | Leu | Leu | Lys | Gln | Arg | Ser | Thr | Gln | Leu | | | | | | |
| | | 595 | | | | | 600 | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3387 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|-----|
| GTCCACGGAAC | TCCTCAACAG | CGCCTCCTTC | AGCTCCACAG | CCAACACGCC | TCACACAGCA | 60 |
| AAGCCTACCC | CCGCGCCGCG | CCCTGCCCGC | CGCTGCGATG | CTCGCCCGCG | CCCTGCTGCT | 120 |
| GTGCGCGGTC | CTGCGGCTCA | GCCATACAGC | AAATCCTTGC | TGTTCCACCC | CATGTCAAAA | 180 |
| CCGAGGTGTA | TGTATGAGTG | TGGGATTTGA | CCAGTATAAG | TGCGATTGTA | CCCGGACAGG | 240 |
| ATTCTATGGA | GAAAACTGCT | CAACACCGGA | ATTTTGTACA | AGAATAAAAT | TATTTCTGAA | 300 |
| ACCCACTCCA | AACACAATGC | ACTACATACT | TACCCACTTC | AAGGGATTTT | GGAACGTTGT | 360 |
| GAATAACATT | CCCTTCCTTC | GAAATGCAAT | TATGAGTTAT | GTGTTGACAT | CCAGATCACA | 420 |
| TTTGATTGAC | AGTCCACCAA | CTTACAATGC | TGACTATGGC | TACAAAAAGCT | GGAAGGCTTT | 480 |
| CTCTAACCTC | TCCTATTATA | CTAGAGCCCT | TCCTCCTGTG | CCTGATGATT | GCCCGACTCC | 540 |

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| CTTGGGTGTC | AAAGGTAAAA | AGCAGCTTCC | TGATTCAAAAT | GAGATTGTGG | AAAAATTGCT | 600 |
| TCTAAGAAGA | AAGTTCATCC | CTGATCCCCA | GGGCTCAAAAC | ATGATGTTTG | CATTCTTTGC | 660 |
| CCAGCACTTC | ACGCACCAGT | TTTTCAAGAC | AGATCATAAG | CGAGGGCCAG | CTTTCACCAA | 720 |
| CGGGCTGGGC | CATGGGTTGG | ACTTAAATCA | TATTTACGGT | GAAACTCTGG | CTAGACAGCG | 780 |
| TAAACTGCGC | CTTTTCAAGG | ATGGAAAAAT | GAAATATCAG | ATAATTGATG | GAGAGATGTA | 840 |
| TCCTCCACAC | GTCAAAAGATA | CTCAGGCAGA | GATGATCTAC | CCTCCTCAAG | TCCCTGAGCA | 900 |
| TCTACGGTTT | GCTGTGGGGC | AGGAAGTCTT | TGGTCTGTGG | CCTGGTCTGA | TGATGTATGC | 960 |
| CACAATCTGG | CTGGGGGAAC | ACAACAGAGT | ATGTGATGTG | CTTAAACAGG | AGCATCCTGA | 1020 |
| ATGGGGTGAT | GAGCAGTTGT | TCCAGACAAG | CAGGCTAATA | CTGATAGGAG | AGACTATTAA | 1080 |
| GATTGTGATT | GAAGATTATG | TGCAACACTT | GAGTGGCTAT | CACTTCAAAAC | TGAAATTTGA | 1140 |
| CCCAGAACTA | CTTTTCAACA | AACAATTCCA | GTACCAAAAT | CGTATTGCTG | CTGAATTTAA | 1200 |
| CACCCCTCTAT | CACTGGCATC | CCCTTCTGCC | TGACACCTTT | CAAAATTCATG | ACCAGAAATA | 1260 |
| CAACTATCAA | CAGTTTATCT | ACAACAACCTC | TATATTGCTG | GAACATGGA | TTACCCAGTT | 1320 |
| TGTTGAATCA | TTCAACAGGC | AAATTGCTGG | CAGGGTTGCT | GGTGGTAGGA | ATGTTCCACC | 1380 |
| CGCAGTACAG | AAAATATCAC | AGGCTTCCAT | TGACCAGAGC | AGGCAGATGA | AATACCAGTC | 1440 |
| TTTTAATGAG | TACCGCAAAAC | GCTTTATGCT | GAAGCCCTAT | GAATCATTTG | AAGAACCTTAC | 1500 |
| AGGAGAAAAAG | GAAATGTCTG | CAGAGTTGGA | AGCACTCTAT | GGTGACATCG | ATGCTGTGGA | 1560 |
| GCTGTATCCT | GCCCTTCTGG | TAGAAAAAGCC | TGGGCCAGAT | GCCATCTTTG | GTGAAACCAT | 1620 |
| GGTAGAAGTT | GGAGCACCAT | TCTCCTTGAA | AGGACTTATG | GGTAATGTTA | TATGTTCTCC | 1680 |
| TGCCTACTGG | AAGCCAAGCA | CTTTTGGTGG | AGAAATGGGT | TTTCAAAATCA | TCAACACTGC | 1740 |
| CTCAATTACAG | TCTCTCATCT | GCAATAACGT | GAAGGGCTGT | CCCTTTACTT | CATTCAAGTG | 1800 |
| TCCAGATCCA | GAGTCATTA | AAACAGTCAC | CATCAATGCA | AGTTCTTCCC | GCTCCGGACT | 1860 |
| AGATGATATC | AATCCCACAG | TACTACTAAA | AQAACGGTCC | ACTGAACCTGT | AGAAGTCTAA | 1920 |
| TGATCATATT | TATTTATTTA | TATGAACCAT | GTCTATTAAAT | TTAATTATTT | AATAATATTT | 1980 |
| ATATTAAACT | CCTTATGTTA | CTTAACATCT | TCTGTAACAG | AAGTCAGTAC | TCCTGTTGCG | 2040 |
| GAGAAAGGAG | TCATACTTGT | GAAGACTTTT | ATGTCACTAC | TCTAAAGATT | TGCTGTTCGC | 2100 |
| TGTTAAGTTT | GGAAAAACAGT | TTTTATTCTG | TTTTATAAAC | CAGAGAGAAA | TGAGTTTTGA | 2160 |
| CGTCTTTTTA | CTTGAATTTT | AACCTTATAT | ATAAGGACGA | AAGTAAAGAT | GTTTGAATAC | 2220 |
| TTAAACACTA | TCACAAGATG | CCAAAATGCT | GAAAGTTTTT | ACACTGTCGA | TGTTTCCAAT | 2280 |
| GCATCTTCCA | TGATGCATTA | GAAGTAACTA | ATGTTTGAAA | TTTTAAAGTA | CTTTTGGGTA | 2340 |
| TTTTTCTGTC | ATCAAAACAAA | ACAGGTATCA | GTGCATTATT | AAATGAATAT | TTAAATTAGA | 2400 |
| CATTACCAGT | AATTTATGTT | CTACTTTTTA | AAATCAGCAA | TGAAACAATA | ATTTGAAATT | 2460 |
| TCTAAATTCA | TAGGGTAGAA | TCACCTGTAA | AAGCTTGTTT | GATTTCTTAA | AGTTATTAAA | 2520 |
| CTTGACATA | TACCAAAAAAG | AAGCTGTCTT | GGATTTAAAT | CTGTAAAATC | AGATGAAATT | 2580 |
| TTACTACAAT | TGCTTGTAA | AATATTTTAT | AAATGATGTT | CCTTTTTTAC | CAAGAGTATA | 2640 |
| AACCTTTTTA | GTGTGACTGT | TAAAACCTCC | TTTTAAATCA | AAATGCCAAA | TTTATTAAGG | 2700 |
| TGGTGGAGCC | ACTGCAGTGT | TATCTCAAAA | TAAGAATATC | CTGTTGAGAT | ATTCAGAAAT | 2760 |
| CTGTTTATAT | GGCTGGTAAC | ATGTAAAAAC | CCCATAACCC | CGCCAAAAGG | GGTCTTACCC | 2820 |
| TTGAACATAA | AGCAATAACC | AAAAGAGAAA | AGCCCAAAAT | ATTGTTTCCA | AATTTAGGOT | 2880 |
| TTAAACTTTT | TGAAGCAAAAC | TTTTTTTTAG | CCTTGTCAC | TGCAGACCTG | GTAETCAGAT | 2940 |

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TTTGCTATGA GGTAAATGAA GTACCAAGCT GTGCTTGAAT AACGATATGT TTTCTCAGAT 3000
TTTCTGTTGT ACAGTTTAAT TTAGCACTCC ATATCACATT GCAAAAAGTAG CAATGACCTC 3060
ATAAAATACC TCTTCAAAAT GCTTAAATTC ATTTACACACA TTAATTTTAT CTCAGTCTTG 3120
AAGCCAATTC AGTAGGTGCA TTGGAATCAA GCCTGGCTAC CTGCATGCTG TTCCTTTTCT 3180
TTTCTTCTTT TAGCCATTTT GCTAAGAGAC ACAGTCTTCT CAAACACTTC GTTCTCCTA 3240
TTTTTTTTTA CTAGTTTTAA GATCAGAGTT CACTTTCTTT GGACTCTGCC TATATTTTCT 3300
TACCTGAAGT TTTGCAAOTT TTCAGGTAAA CCTCAGCTCA GGACTGCTAT TTAGCTCCTC 3360
TTAAGAAGAT TAAAAAAAAA AAAAAAG 3387

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(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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CCTTCCTTCG AAATGCAATT A 21
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(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
AAACTGATGC GTGAAGTGCT G 21
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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
GAGATTGTGG GAAAAATTGCT T 21
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